

WEST Search History

DATE: Thursday, July 06, 2006

Hide?	Set Name	Query	Hit Count
	<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=AND</i>		
<input type="checkbox"/>	L11	l2 and l9	20
<input type="checkbox"/>	L10	l1 and L9	21
<input type="checkbox"/>	L9	l6 or l7 or L8	270
<input type="checkbox"/>	L8	edward.in. and thayer.in.	82
<input type="checkbox"/>	L7	philippa.in. and webster.in.	10
<input type="checkbox"/>	L6	james.in. and holloway.in.	186
<input type="checkbox"/>	L5	glycoprotein near hormone-1	3
<input type="checkbox"/>	L4	L2 and mammalian	17423
<input type="checkbox"/>	L3	l2 and mannalian	15
<input type="checkbox"/>	L2	l1 and hormone	25603
<input type="checkbox"/>	L1	glycoprotein	56365

END OF SEARCH HISTORY

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 16:57:28 ON 06 JUL 2006

=> file medline, biosis, caplus

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 16:57:47 ON 06 JUL 2006

FILE 'BIOSIS' ENTERED AT 16:57:47 ON 06 JUL 2006

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FILE 'CAPLUS' ENTERED AT 16:57:47 ON 06 JUL 2006

USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.

PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

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=> glycoprotein hormone-1

L1 1 GLYCOPROTEIN HORMONE-1

=> glycoprotein

L2 430089 GLYCOPROTEIN

=> l2 and hormone

L3 17285 L2 AND HORMONE

=> glycoprotein hormone

L4 5623 GLYCOPROTEIN HORMONE

=> l4 and 1970-2000/py

L5 4454 L4 AND 1970-2000/PY

=> james?/au and holloway?/au

L6 307 JAMES?/AU AND HOLLOWAY?/AU

=> philippa?/au and webster?/au

L7 0 PHILIPPA?/AU AND WEBSTER?/AU

=> edward?/au and thayer?/au

L8 287 EDWARD?/AU AND THAYER?/AU

=> l6 or l8

L9 594 L6 OR L8

=> l5 and l9

L10 0 L5 AND L9

=> d his

(FILE 'HOME' ENTERED AT 16:57:28 ON 06 JUL 2006)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 16:57:47 ON 06 JUL 2006

L1 1 GLYCOPROTEIN HORMONE-1

L2 430089 GLYCOPROTEIN

L3 17285 L2 AND HORMONE

L4 5623 GLYCOPROTEIN HORMONE

L5 4454 L4 AND 1970-2000/PY

L6 307 JAMES?/AU AND HOLLOWAY?/AU

L7 0 PHILIPPA?/AU AND WEBSTER?/AU

L8 287 EDWARD?/AU AND THAYER?/AU

L9 594 L6 OR L8

L10 0 L5 AND L9

=> logoff

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OM protein - protein search, using sw model

Run on: June 26, 2006, 09:18:28 ; Search time 200 Seconds
(without alignments)
297.191 Million cell updates/sec

Title: US-10-733-597-2
Perfect score: 722
Sequence: 1 MKLAFLFLGPMALLLLAGYG.....VAIRCDGACSTATTECETI 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
		Query					
Result	No.	Score	Match	Length	DB ID	Description	
	1	722	100.0	130	4 AAG63211	Aag63211 Amino aci	
	2	722	100.0	130	4 AAG64064	Aag64064 Human ant	
	3	722	100.0	130	4 AAE09440	Aae09440 Human sbg	
	4	722	100.0	130	5 AAU97612	Aau97612 Human OGH	
	5	722	100.0	130	5 AAU96153	Aau96153 Human BRP	
	6	722	100.0	130	5 AAU10366	Aau10366 Human bet	
	7	722	100.0	130	6 ABG74206	Abg74206 Human gly	

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:14:53 ; Search time 39.661 Seconds
(without alignments)
286.906 Million cell updates/sec

Title: US-10-733-597-2
Perfect score: 722
Sequence: 1 MKLAFLFLGPMALLLLAGYG.....VAIRCDCGACSTATTECETI 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result		Query						
No.	Score	Match	Length	DB	ID	Description		
1	521	72.2	118	3	US-10-162-335-26	Sequence 26, Appl		
2	178	24.7	149	1	US-08-425-673-5	Sequence 5, Appli		
3	178	24.7	203	2	US-09-059-625-88	Sequence 88, Appl		
4	170	23.5	104	2	US-08-918-288-74	Sequence 74, Appl		
5	170	23.5	104	2	US-09-282-357-74	Sequence 74, Appl		
6	170	23.5	108	2	US-08-918-288-73	Sequence 73, Appl		
7	170	23.5	108	2	US-09-282-357-73	Sequence 73, Appl		
8	170	23.5	111	2	US-08-918-288-72	Sequence 72, Appl		
9	170	23.5	111	2	US-09-282-357-72	Sequence 72, Appl		
10	164.5	22.8	242	2	US-09-059-625-74	Sequence 74, Appl		

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OM protein - protein search, using sw model

Run on: June 26, 2006, 09:18:48 ; Search time 72 Seconds
 (without alignments)
 836.360 Million cell updates/sec

Title: US-10-733-597-2
 Perfect score: 722
 Sequence: 1 MKLAFLFLGPMALLLLAGYG.....VAIRCDCGACSTATTECETI 130

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	722	100.0	130	3	US-09-818-954A-1	Sequence 1, Appli
2	722	100.0	130	3	US-09-943-388-2	Sequence 2, Appli
3	722	100.0	130	3	US-09-943-388-5	Sequence 5, Appli
4	722	100.0	130	3	US-09-927-876-81	Sequence 81, Appli
5	722	100.0	130	4	US-10-196-437A-5	Sequence 5, Appli
6	722	100.0	130	4	US-10-168-048A-1	Sequence 1, Appli
7	722	100.0	130	4	US-10-203-708-27	Sequence 27, Appli
8	722	100.0	130	4	US-10-449-140-1	Sequence 1, Appli
9	722	100.0	130	4	US-10-373-617A-9	Sequence 9, Appli
10	722	100.0	130	4	US-10-360-149-81	Sequence 81, Appli
11	722	100.0	130	4	US-10-457-047-81	Sequence 81, Appli

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:16:57 ; Search time 14.322 Seconds
 (without alignments)
 207.367 Million cell updates/sec

Title: US-10-733-597-2
 Perfect score: 722
 Sequence: 1 MKLAFLEFLGPMALLLLAGYG.....VAIRCDCGACSTATTECETI 130

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_New:*
 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query					Description
	Score	Match Length	DB	ID		
1	164	22.7	129	7	US-11-183-218-14	Sequence 14, Appl
2	155	21.5	165	6	US-10-915-763A-14	Sequence 14, Appl
3	155	21.5	165	7	US-11-183-218-72	Sequence 72, Appl
4	143	19.8	145	7	US-11-273-478-2	Sequence 2, Appli
5	92	12.7	38	7	US-11-243-438-24	Sequence 24, Appl
6	82	11.4	348	6	US-10-449-902-34800	Sequence 34800, A
7	78.5	10.9	469	7	US-11-246-999-41	Sequence 41, Appl
8	78.5	10.9	494	7	US-11-246-999-30	Sequence 30, Appl
9	78.5	10.9	567	7	US-11-246-999-50	Sequence 50, Appl

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:08:22 ; Search time 26.9915 Seconds
(without alignments)
463.411 Million cell updates/sec

Title: US-10-733-597-2
Perfect score: 722
Sequence: 1 MKLAFLFLGPMALLLLAGYG.....VAIRCDCGACSTATTECETI 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	No.	Score	Match	Length	ID	
1	210	29.1	141	1	UTBOB	lutropin beta chai
2	209	28.9	144	1	UTCAB	gonadotropin beta
3	207	28.7	141	1	B60626	gonadotropin beta
4	207	28.7	146	1	S16763	gonadotropin beta
5	204.5	28.3	141	1	UTSHB	lutropin beta chai
6	201.5	27.9	140	2	A48166	gonadotropin II be
7	201	27.8	142	1	C36179	gonadotropin II be
8	199	27.6	136	2	I50554	gonadotropin II be
9	198	27.4	113	1	S07092	gonadotropin beta
10	192	26.6	142	2	I51232	gonadotropin II be
11	189	26.2	112	2	S21196	lutropin beta chai
12	189	26.2	147	2	I50994	gonadotropin II be
13	186.5	25.8	142	2	I50143	gonadotropin II be

OM protein - protein search, using sw model

Run on: June 23, 2006, 20:03:21 ; Search time 212.627 Seconds
 (without alignments)
 565.554 Million cell updates/sec

Title: US-10-733-597-2
 Perfect score: 722
 Sequence: 1 MKLAFLFLGPMALLLLAGYG.....VAIRCDCGACSTATTECETI 130

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	722	100.0	130	1	GPHB5_HUMAN Q86yw7 homo sapien
2	636	88.1	130	1	GPHB5_MOUSE Q812b2 mus musculu
3	619.5	85.8	129	2	Q5VJF5_RAT Q5vjf5 rattus norv
4	590	81.7	115	2	Q2NL39_MOUSE Q2nl39 mus musculu
5	440	60.9	99	2	Q4S6H4_TETNG Q4s6h4 tetraodon n
6	428	59.3	124	2	Q4S0U3_TETNG Q4s0u3 tetraodon n
7	213.5	29.6	149	1	GTHB2_CLUPA Q9ygh2 clupea pall
8	211	29.2	128	2	Q5YFS0_ACIGU Q5yfs0 acipenser g
9	211	29.2	128	2	Q9I997_ACIBE Q9i997 acipenser b
10	210	29.1	140	2	Q5UK78_BRARE Q5uk78 brachydanio
11	210	29.1	140	2	Q6TCF5_BRARE Q6tcf5 brachydanio
12	210	29.1	141	1	LSHB_BOVIN P04651 bos taurus
13	209	28.9	140	1	GTHB2_CARAU Q98849 carassius a
14	209	28.9	144	1	GTHB2_CYPKA P01235 cyprinus ca
15	208	28.8	122	2	Q306L6_9TELE Q306l6 pimephales

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OM protein - protein search, using sw model

Run on: June 26, 2006, 09:22:24 ; Search time 83 Seconds
(without alignments)
583.915 Million cell updates/sec

Title: US-10-733-597-9
Perfect score: 600
Sequence: 1 ASSGNLRTFVGCAVREFTFL.....VAIRCDCGACSTATTECETI 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	600	100.0	106	4 AAG64065	Aag64065 Human ant
2	600	100.0	106	5 AAU96154	Aau96154 Human mat
3	600	100.0	106	6 ABP72423	Abp72423 Human gly
4	600	100.0	106	8 ADF72484	Adf72484 Mature hu
5	600	100.0	106	9 ADW86161	Adw86161 Human Zlu
6	600	100.0	106	9 AEC83182	Aec83182 Human mat
7	600	100.0	129	5 AAU96157	Aau96157 Human BRP

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:14:53 ; Search time 32.339 Seconds
(without alignments)
286.906 Million cell updates/sec

Title: US-10-733-597-9
Perfect score: 600
Sequence: 1 ASSGNLRTFVGCAVREFTFL.....VAIRCDCGACSTATTECETI 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	521	86.8	118	3	US-10-162-335-26	Sequence 26, Appl
2	178	29.7	149	1	US-08-425-673-5	Sequence 5, Appli
3	170	28.3	104	2	US-08-918-288-74	Sequence 74, Appl
4	170	28.3	104	2	US-09-282-357-74	Sequence 74, Appl
5	170	28.3	108	2	US-08-918-288-73	Sequence 73, Appl
6	170	28.3	108	2	US-09-282-357-73	Sequence 73, Appl
7	170	28.3	111	2	US-08-918-288-72	Sequence 72, Appl
8	170	28.3	111	2	US-09-282-357-72	Sequence 72, Appl
9	164	27.3	97	2	US-10-099-322-299	Sequence 299, App
10	164	27.3	97	2	US-10-044-564-299	Sequence 299, App

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OM protein - protein search, using sw model

Run on: June 26, 2006, 09:23:34 ; Search time 67 Seconds
(without alignments)
732.847 Million cell updates/sec

Title: US-10-733-597-9
Perfect score: 600
Sequence: 1 ASSGNLRTFVGCAVREFTFL.....VAIRCDCGACSTATTECETI 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 59

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	600	100.0	106	3	US-09-818-954A-3	Sequence 3, Appli
2	600	100.0	106	3	US-09-943-388-9	Sequence 9, Appli
3	600	100.0	106	3	US-09-927-876-83	Sequence 83, Appl
4	600	100.0	106	4	US-10-196-437A-6	Sequence 6, Appli
5	600	100.0	106	4	US-10-168-048A-5	Sequence 5, Appli
6	600	100.0	106	4	US-10-449-140-3	Sequence 3, Appli
7	600	100.0	106	4	US-10-360-149-83	Sequence 83, Appl
8	600	100.0	106	4	US-10-457-047-83	Sequence 83, Appl
9	600	100.0	106	4	US-10-459-000A-6	Sequence 6, Appli
10	600	100.0	106	5	US-10-733-597-9	Sequence 9, Appli
11	600	100.0	106	5	US-10-811-081-83	Sequence 83, Appl

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:16:57 ; Search time 11.678 Seconds
(without alignments)
207.367 Million cell updates/sec

Title: US-10-733-597-9
Perfect score: 600
Sequence: 1 ASSGNLRTFVGCAVREFTFL.....VAIRCDGACSTATTECETI 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	164	27.3	129	7	US-11-183-218-14	Sequence 14, Appl
2	143	23.8	145	7	US-11-273-478-2	Sequence 2, Appli
3	143	23.8	165	6	US-10-915-763A-14	Sequence 14, Appl
4	143	23.8	165	7	US-11-183-218-72	Sequence 72, Appl
5	92	15.3	38	7	US-11-243-438-24	Sequence 24, Appl
6	82	13.7	348	6	US-10-449-902-34800	Sequence 34800, A
7	76.5	12.8	257	6	US-10-449-902-36378	Sequence 36378, A
8	71.5	11.9	376	6	US-10-449-902-53472	Sequence 53472, A
9	65	10.8	368	6	US-10-449-902-30253	Sequence 30253, A

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:08:22 ; Search time 22.0085 Seconds
(without alignments)
463.411 Million cell updates/sec

Title: US-10-733-597-9
Perfect score: 600
Sequence: 1 ASSGNLRTFVGCAVREFTFL.....VAIRCDCGACSTATTECETI 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	209	34.8	144	1	UTCAB	gonadotropin beta	
2	207	34.5	141	1	B60626	gonadotropin beta	
3	207	34.5	146	1	S16763	gonadotropin beta	
4	201	33.5	141	1	UTBOB	lutropin beta chai	
5	201	33.5	141	1	UTSHB	lutropin beta chai	
6	199	33.2	136	2	I50554	gonadotropin II be	
7	199	33.2	140	2	A48166	gonadotropin II be	
8	199	33.2	142	1	C36179	gonadotropin II be	
9	198	33.0	113	1	S07092	gonadotropin beta	
10	191	31.8	142	2	I51232	gonadotropin II be	
11	189	31.5	112	2	S21196	lutropin beta chai	
12	189	31.5	147	2	I50994	gonadotropin II be	
13	186	31.0	142	2	I50143	gonadotropin II be	

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:03:21 ; Search time 173.373 Seconds
(without alignments)
565.554 Million cell updates/sec

Title: US-10-733-597-9
Perfect score: 600
Sequence: 1 ASSGNLRTFVGCAVREFTFL.....VAIRCDCGACSTATTECETI 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	600	100.0	130	1	GPHB5_HUMAN	Q86yw7	homo sapien
2	577	96.2	115	2	Q2NL39_MOUSE	Q2nl39	mus musculu
3	577	96.2	130	1	GPHB5_MOUSE	Q812b2	mus musculu
4	576	96.0	129	2	Q5VJF5_RAT	Q5vjf5	rattus norv
5	440	73.3	99	2	Q4S6H4_TETNG	Q4s6h4	tetraodon n
6	409	68.2	124	2	Q4S0U3_TETNG	Q4s0u3	tetraodon n
7	211	35.2	128	2	Q5YFS0_ACIGU	Q5yfs0	acipenser g
8	211	35.2	128	2	Q9I997_ACIBE	Q9i997	acipenser b
9	209	34.8	140	1	GTHB2_CARAU	Q98849	carassius a
10	209	34.8	144	1	GTHB2_CYPCA	P01235	cyprinus ca
11	208	34.7	122	2	Q306L6_9TELE	Q306l6	pimephales
12	208	34.7	128	2	Q6PV99_ACISC	Q6pv99	acipenser s
13	207	34.5	140	2	Q98TY3_MYLPI	Q98ty3	mylopharyng
14	207	34.5	141	1	GTHB2_HYPMO	P37038	hypophthalm
15	207	34.5	146	1	GTHB2_CTEID	P30984	ctenopharyn